

- 63 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Levy, Gary
- (ii) TITLE OF INVENTION: Methods of Modulating Immune Coagulation
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: BERESKIN & PARR
 - (B) STREET: 40 King Street West
 - (C) CITY: Toronto
 - (D) STATE: Ontario
 - (E) COUNTRY: Canada
 - (F) ZIP: M5H 3Y3
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Gravelle, Micheline
 - (B) REGISTRATION NUMBER: 40,261
 - (C) REFERENCE/DOCKET NUMBER: 9579-006
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (416) 364-7311
 - (B) TELEFAX: (416) 361-1398

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATCTAGGGT TGGAAAGCCAG GTCTCCTGAG TATGCGAGAA TAAATACAGT CATGGAAGTG	60
TAAAGAGTCT GCCAACATTT TGAGAAATGTG AATAGGATTT GGCTAAAATT AAGGGGATAT	120
ACAGAAAAAGT CATAGGAAAT CAGGTTAAAG ACATAAAATAT GAGATAGGCT ACAGAGTGTT	180
TTAAGTAATA CAATAAAACA TTTAGATTTTG TGCCCATGTC AGTCATTTTG AAATTATTTT	240
TAAAGCAAAA AAACCCTTTT TAAACAAGAA ATCTTATGAG ATGTCAATAT GCAAAACAAA	300
TTAAAAGGAG GTGGTTCTC TAACTGAAGC TGTTCCCTCTT TCCTGCCTTC AGCCTCTGAA	360

- 64 -

GAGAAAGTTA GAAAATATT ATCATTAATG CTACATGTTT TGAACAAGCT GATATAACAA	420
GTGGCCCAGA GAGCAGGTAG AAGAACCCAGC GTGGAGACAG AAAGCAAGAG GCCCCCTGC	480
CAGGGCTACC TGCAGAAAGA AAGGGCAAAG ATGCTGTAGG CAAGAGAAGT TCAGGACAGA	540
CACTGGCATA GCTCAAAGAT TCACATTTGA GCAGCTGTGG AAGATGACAG TACAATTACC	600
AAAATGTCGA AGGGCAAAGG AGGCAGCTAC TGGTTTGAT GAAAGACAAT TATGTCCTTT	660
TAAATGGGTC TTAGACATTT AGACATTTAT ATACACTATG CTACGGACAA AGGAATAGAA	720
AGTAGCACTT TTTTCTCCAC TAGTTTCTT CTCTTTTCA AGTAGATGAA GCAAAAGTCA	780
ACTGCAATAG TCAGAAAGCT GTACTTTGTT ACACCTAGAA ACTTCTAAAA GTGCTTAAGA	840
TTTCACCTGA AAGTCCAACA TGAAGAAAAT ACAGGCTCCC CAATGCCCA TTCTAAGAAG	900
GAAAAAGGAC CATTTCATT TTAGTAACGT TTCTGTTCTA TAGACAGTTT GGATAACTAG	960
CTCTTACTTT TTATCTTAA AACTGTTTT TCCAGTGAAG TTACGTATAA TTATTTACTT	1020
CAAGCGTAGT ATACCAAATT ACTTTAGAAA TGCAAGACTT TTCTTATACT TCATAAAATA	1080
CATTATGAAA GTGAATCTTG TTGGCTGTGT ACATTTGACT ATAATAATTT CAATGCATAT	1140
TATTTCTATT GAGAGTAAGT TACAGTTTT GGCAAACCTGC GTTTGATGAG GGCTATCTCC	1200
TCTTCCTGTG CGTTTCTAAA ACTTGTGATG CAAACGCTCC CACCCCTTCC TGGGAACACA	1260
GAAAGCCTGA CTCAGGCCAT GGCGCTATT AAAGCAGCTC CAGCCCTGCG CACTCCCTGC	1320
TGGGGTGAGC AGCACTGTAA AGATGAAGCT GGCTAACTGG TACTGGCTGA GCTCAGCTGT	1380
TCTTGCCACT TACGGTTTT TGGTTGTGGC AAACAATGAA ACAGAGGAAA TTAAAGATGA	1440
AAGAGCAAAG GATGTCTGCC CAGTGAGACT AGAAAGCAGA GGGAAATGCG AAGAGGCAGG	1500
GGAGTGCCCC TACCAAGGTA GCCTGCCCTT CTTGACTATT CAGCTCCCGA AGCAATTTCAG	1560
CAGGATCGAG GAGGTGTTCA AAGAAGTCCA AAACCTCAAG GAAATCGTAA ATAGTCTAAA	1620
GAAATCTTGC CAAGACTGCA AGCTGCAGGC TGATGACAAC GGAGACCCAG GCAGAAACGG	1680
ACTGTTGTTA CCCAGTACAG GAGCCCCGGG AGAGGTTGGT GATAACAGAG TTAGAGAATT	1740
AGAGAGTGAG GTTAACAAGC TGTCCTCTGA GCTAAAGAAT GCCAAAGAGG AGATCAATGT	1800
ACTTCATGGT CGCCTGGAGA AGCTGAATCT TGTAAATATG AACAAACATAG AAAATTATGT	1860
TGACAGCAA GTGGCAAATC TAACATTTGT TGTCAATAGT TTGGATGGCA AATGTTCAA	1920
GTGTCCCAGC CAAGAACAAA TACAGTCACG TCCAGGTATG TATAATAATG TTTTCTTATC	1980
ATATGTTCAT AAATGTTATA CAGTCAGAGA TGTATCTAAA AGATTAACCT GAGTCAGTAA	2040
GTAAATAGA TGACAGATTA AGTCTTTAT TTATCAAGGT GCACAGGAAA AAATAAATAT	2100
CTTCTCAAAT ATGACCACAT AAATATGACC TAATTACAAA ATCATAGTTA GTTCTGTATC	2160
CACTGGAAAGT CACTTTCAAT TTTAAGATCT TATTTGTAA TGCCAGACCT ACTTGCAAGC	2220
AGAGATTAGA GGTCTTTCT GCTTTATAAC ATTAGGTTCT TCTTGTGAGG CCTTAAGCAT	2280
TTACTAAACA CCTTCAAGTA AGTTTAGTAA AGTTTCATTA CTGCCATTGA TTCAATTATC	2340

- 65 -

AAACTGCTTT	TGTACATATA	AAGAATTCTT	CAGATGCATG	GTTTCTATTA	ACAAGATCCA	2400
ATGCCTTCCT	TTTATTCCC	CTTCAGTTCA	ACATCTAATA	TATAAAGATT	GCTCTGACTA	2460
CTACGCAATA	GGCAAAGAA	GCAGTGAGAC	CTACAGAGTT	ACACCTGATC	CCAAAAATAG	2520
TAGCTTGAA	GTTTACTGTG	ACATGGAGAC	CATGGGGGA	GGCTGGACAG	TGCTGCAGGC	2580
ACGTCTCGAT	GGGAGCACCA	ACTTCACCAAG	AACATGGCAA	GAETACAAAG	CAGGCTTTGG	2640
AAACCTCAGA	AGGGAATT	GGCTGGGGAA	CGATAAAATT	CATCTTCTGA	CCAAGAGTAA	2700
GGAAATGATT	CTGAGAATAG	ATCTTGAAGA	CTTTAATGGT	GTCGAACATAT	ATGCCTTGTA	2760
TGATCAGTTT	TATGTGGCTA	ATGAGTTCT	CAAATATCGT	TTACACGTTG	GTAACATATAA	2820
TGGCACAGCT	GGAGATGCAT	TACGTTCAA	CAAACATTAC	AACCACGATC	TGAAGTTTT	2880
CACCACTCCA	GATAAAGACA	ATGATCGATA	TCCTTCTGGG	AACTGTGGC	TGTACTACAG	2940
TTCAGGCTGG	TGGTTTGATG	CATGTCTTC	TGCAAACCTTA	AATGGCAAAT	ATTATCACCA	3000
AAAATACAGA	GGTGTCCGTA	ATGGGATT	CTGGGGTACC	TGGCCTGGTG	TAAGTGAGGC	3060
ACACCCCTGGT	GGCTACAAGT	CCTCCCTCAA	AGAGGCTAAG	ATGATGATCA	GACCCAAGCA	3120
CTTTAAGCCA	AAAATCACTC	TGTTCATTC	TCCAGGTATT	CGTTATCTAA	TAGGGCAATT	3180
AATTCCCTGT	TTCATATT	TCATAGCTAA	AAAATGATGT	CTGACGGCTA	GGTTCTTATG	3240
CTACACAGCA	TTTGAATAA	AGCTGAAAAA	CAATGCATTT	TAAAGGAGTC	CTTTGTTGTT	3300
ATGCTGTTAT	CCAATGAACA	CTTGCAGCA	ATTAGCAATA	TTGAGAATTA	TACATTAGAT	3360
TTACAATTCT	TTTAATTCT	ATTGAAACCTT	TTTCTATTGC	TTGTATTACT	TGCTGTATTT	3420
AAAAAATAAT	TGTTGGCTGG	GTGTGGTAGC	TCACGCCTGT	AATCCCAGCA	CTTTGGAATG	3480
TCAAGGCAGG	CAGATCACTT	GAGGTCAAGGA	GTTTGAGACC	AGCCTGGCCA	AACATGTGAA	3540
ACGCTGTCTC	TATTAATAA	ACAAAAATTA	GCCGGGCATG	GTGGTACATG	CCTGTAATCA	3600
ACGCTGTTA	TTAAAAATAC	AAAAATTAGC	CGGGCATGGT	GGACATGCC	GTAATCCTAG	3660
TACTTGGGAG	GCTGAGGCAG	GAGAATCGCT	TGAACCTGAG	AGGAAGAGGT	TGCAGTGAGC	3720
CAAGAATGAG	CCACTGCACT	CCAGCATGGG	TGACAGAGAA	AACTCTGTCT	CAAACAAAAA	3780
AATAATAAAA	TTTATTCACT	AGGTGGATTC	TACACAAAGT	AATCTGTATT	TGGGCCATGA	3840
TTTAAGCACA	TCTGAAGGTA	TATCACTCTT	TTCAGGCTAT	AATTATTG	GTAATCTTCA	3900
TTCTGAGACA	AACTTAATCT	ATATCATT	CTTGCAACA	GAACAACCT	ACAGCATT	3960
GGTTCCCAGA	CTAAGGAAC	TAATATCTAT	ATAATTAAAC	TTGTTCATTT	ATCATTGATG	4020
AAATATAAAA	TACTTGTCA	TTAACCGTT	AAAAATGTG	GTAGCATAAT	GTCACCCCAA	4080
AAAGCATTCA	GAAAGCAATG	TAACTGTGAA	GACCAGGGTT	TAAAGGTAAT	TCATTTATAG	4140
TTTATAACTC	CTTAGATGTT	TGATGTTGAA	AACTGCTTTA	ACATGAAAAT	TATCTTCTC	4200
TGCTCTGTGT	GAACAATAGC	TTTAATT	AGATTGCTCA	CTACTGTACT	AGACTACTGG	4260
TAGGTTTTTT	TGGGGGGGGG	TGGGTAGGG	TATGTGGGTA	ATGAAGCATT	TACTTACAGG	4320

- 66 -

CTATCATACT CTGAGGCCAA	TTTATCTCC AAAGCAATAA	TATCATTAAG TGATTCACTT	4380
CATAGAACGC TAAGTTCTC	TAGGACAGAT AGAAAACATG	AATTTTGAAA TATATAGAAC	4440
AGTAGTTAAA ATACTATATA	TTTCAACCCT GGCTGGTAGA	TTGCTTATTT TACTATCAGA	4500
AACTAAAAGA TAGATTTTA CCCAACAGA	AGTATCTGTA ATTTTATAA	TTCATCAATT	4560
CTGGAATGCT ATATATAATA	TTTAAAAGAC TTTTTAAATG	TGTTTAATTT CATCATCGTA	4620
AAAAGGGATC			4630

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Leu Ala Asn Trp Tyr Trp	Leu Ser Ser Ala Val	Leu Ala Thr	
1 5	10	15	
Tyr Gly Phe Leu Val Val Ala Asn Asn	Glu Thr Glu Glu Ile Lys Asp		
20	25	30	
Glu Arg Ala Lys Asp Val Cys Pro Val Arg Leu Glu Ser Arg Gly Lys			
35 40	45		
Cys Glu Glu Ala Gly Glu Cys Pro Tyr Gln Val Ser Leu Pro Pro Leu			
50 55	60		
Thr Ile Gln Leu Pro Lys Gln Phe Ser Arg Ile Glu Glu Val Phe Lys			
65 70	75	80	
Glu Val Gln Asn Leu Lys Glu Ile Val Asn Ser Leu Lys Ser Cys			
85 90	95		
Gln Asp Cys Lys Leu Gln Ala Asp Asp Asn Gly Asp Pro Gly Arg Asn			
100 105	110		
Gly Leu Leu Leu Pro Ser Thr Gly Ala Pro Gly Glu Val Gly Asp Asn			
115 120	125		
Arg Val Arg Glu Leu Glu Ser Glu Val Asn Lys Leu Ser Ser Glu Leu			
130 135	140		
Lys Asn Ala Lys Glu Glu Ile Asn Val Leu His Gly Arg Leu Glu Lys			
145 150	155	160	
Leu Asn Leu Val Asn Met Asn Asn Ile Glu Asn Tyr Val Asp Ser Lys			
165 170	175		
Val Ala Asn Leu Thr Phe Val Val Asn Ser Leu Asp Gly Lys Cys Ser			
180 185	190		
Lys Cys Pro Ser Gln Glu Gln Ile Gln Ser Arg Pro Val Gln His Leu			
195 200	205		
Ile Tyr Lys Asp Cys Ser Asp Tyr Tyr Ala Ile Gly Lys Arg Ser Ser			
210 215	220		

- 67 -

Glu Thr Tyr Arg Val Thr Pro Asp Pro Lys Asn Ser Ser Phe Glu Val
 225 230 235 240
 Tyr Cys Asp Met Glu Thr Met Gly Gly Gly Trp Thr Val Leu Gln Ala
 245 250 255
 Arg Leu Asp Gly Ser Thr Asn Phe Thr Arg Thr Trp Gln Asp Tyr Lys
 260 265 270 275
 Ala Gly Phe Gly Asn Leu Arg Arg Glu Phe Trp Leu Gly Asn Asp Lys
 275 280 285
 Ile His Leu Leu Thr Lys Ser Lys Glu Met Ile Leu Arg Ile Asp Leu
 290 295 300
 Glu Asp Phe Asn Gly Val Glu Leu Tyr Ala Leu Tyr Asp Gln Phe Tyr
 305 310 315 320
 Val Ala Asn Glu Phe Leu Lys Tyr Arg Leu His Val Gly Asn Tyr Asn
 325 330 335
 Gly Thr Ala Gly Asp Ala Leu Arg Phe Asn Lys His Tyr Asn His Asp
 340 345 350
 Leu Lys Phe Phe Thr Thr Pro Asp Lys Asp Asn Asp Arg Tyr Pro Ser
 355 360 365
 Gly Asn Cys Gly Leu Tyr Tyr Ser Ser Gly Trp Trp Phe Asp Ala Cys
 370 375 380
 Leu Ser Ala Asn Leu Asn Gly Lys Tyr Tyr His Gln Lys Tyr Arg Gly
 385 390 395 400
 Val Arg Asn Gly Ile Phe Trp Gly Thr Trp Pro Gly Val Ser Glu Ala
 405 410 415
 His Pro Gly Gly Tyr Lys Ser Ser Phe Lys Glu Ala Lys Met Met Ile
 420 425 430
 Arg Pro Lys His Phe Lys Pro
 435

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5403 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: other nucleic acid
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3.

AGGCCT GTCTGACAAA TTCTTCATAC ACACATTTCC

ATAGGTTATT TCTATAGGAG AAAAAAAATA TTCAAATTCC TTGTGCAC TG GTAACAGGCA 120
TGAAGGCTCA GC~~AA~~AGCCAA TACGTGTTAT GTCCAGTTGG AGACAGTGCC AGGGCCAACA 180
TTCCAGACTT CTCAGATAGA AAGTGCGCCT GCCTGCCCTG CTCTGAGAAT TTGAAGAGAG 240
TAGTTCAGTT AGAATTAAGA GGCAGTAGAG AAAAGTCTTG GGAAATCTGG TTAGAGATAT 300
AAAATATGAGA ACTGGACATG GTGGTACACA CCTGTGATCT CTGTGTTAG GAGGGAGAGG 360

- 68 -

CAGAGAGATC AGGAGTTCAA GGCCAGCCTG AGCTACTTGA GACCCAGTCT AAATAAATAA	420
GAGATAGATT ACAGAGTGCC TTTAACTAGT ACAGAGAAAG AATTTGGGTT TATCTGTGTC	480
AGTTACGCTG AAATAATTT TAAGTAATAA AATCCCTTT AATAAGAAC CTTATGAGGT	540
CAGTATGCAC AATGAACCTA AGAGAGACCC CCAGCTCCTG AGCTGAGTGA TGGGAAAGGA	600
CAGCCACTGC CTGTGATGTG TGAGTGACGT GCTTCCAAGT GTTTAACCA CTGACGATTA	660
CATAGCCTGC ACAGTCAGGA GAAAACAGCC GTATTCTCTG CCAGTTCTCT TCCCTTTAC	720
AAACAGATGA GAGACACACA CAGAGAATCC ATTTAAAGAG CGGACCTTG TTCTGATTAG	780
GGGCAATTT AAGTACTTAA GAGTCACAC AAAGTCTAGC CTTCAAAAAG AAAACAGGTT	840
CCCAAACCTAG GGAGGAAACA GAATCATTC CATTGGGTG ACATTTAGTG GGAAGAAGCT	900
CACAGACATT TAGACGTTCC AACTCTTCC CCACTAGTGG ACCAAGTATA TAATATGGTA	960
TCTTTGGGC ACTGGTATTA CAACTGTTT TTAAACAAA GACTTCCCT GTGCTTTACT	1020
AAAAACCCAG ACGGTGAATC TTGAATACAA TGCCTGGCAC CCACGGCAGG CATTCTATTG	1080
TGCATAGTT TGACTGACAG GAGATGACAG CATTGGCTG GCTGCCCTTG CTGAGGACCC	1140
TCTCCTCCTG TGTGGCGTCT GAGACTGTGA TGCAATGCG CCCGCCCTT TCTGGGAACT	1200
CAGAACGCCT GAGTCAGGCG GCGGTGGCTA TTAAAGGCC TGGTCAGGCT GGGCTGCCGC	1260
ACTGCAAGGA TGAGGCTTCC TGGTTGGTTG TGGCTGAGTT CTGCCGTCT CGCTGCCTGC	1320
CGAGCGGTGG AGGAGCACAA CCTGACTGAG GGGCTGGAGG ATGCCAGCGC CCAGGCTGCC	1380
TGCCCGCGA GGCTGGAGGG CAGCGGGAGG TGCAGGGGA GCCAGTGCCT CTTCCAGCTC	1440
ACCCCTGCCCA CGCTGACCAT CCAGCTCCCG CGGCAGCTTG GCAGCATGGA GGAGGTGCTC	1500
AAAGAAAGTGC GGACCCTCAA GGAAGCAGTG GACAGTCTGA AGAAATCTG CCAGGACTGT	1560
AAGTTGCAGG CTGACGACCA TCGAGATCCC GGCGGGATG GAGGGAATGG AGCAGAGACA	1620
GCCGAGGACA GTAGAGTCCA GGAACCTGGAG AGTCAGGTGA ACAAGCTGTC CTCAGAGCTG	1680
AAGAATGCAA AGGACCAGAT CCAGGGCTG CAGGGCGCC TGGAGACGCT CCATCTGGTA	1740
AATATGAAĆA ACATTGAGAA CTACGTGGAC AACAAAGTGG CAAATCTAAC CGTTGTGGTC	1800
AACAGTTGG ATGGCAAGTG TTCCAAGTGT CCCAGCCAAG AACACATGCA GTCACAGCCG	1860
GGTAGGTGTA ATGAGGGTCA TACAGTTGT TCATGAAAGC TGTATAGCCA GATAGTGGCC	1920
ATAAACATTA ACCCGAGGGA GCATAAGTTA GTCAGACTTT CACCTGTTAA GTTATGGCAG	1980
GAGAAACAAG TGTGTTCTCA AATGAGACAA CAGAAATGGT AAATGATCCA CGTACAAAAA	2040
TCCTATTAGT TGTACTCGTT AGAGACCGTC ACTTGCAAGT CTCTAGACCT TCCCTGCTAG	2100
GTCGACCAAC AGACGAGCAG AAACAGATTG CTCCCGGAAT CTGAACACAT ATTTGAACAC	2160
AGGACAGGTA TGGCAAGGTT CCTGGCTCTG CTTGCTTAGG TCCCTGGAA TCAGATCTT	2220
GGTGGCTGAT GGGCTTTATA AGGCTTCAC AAACAATCTG CTGTGCTAGG TTCTCAAATA	2280
TCTAGTGAGA ATGGGAGATT TTTATACATG GAAGCATCTC TCCTCTCTCT CTCCTCTCTC	2340

- 69 -

CTCTCTCTTC	TCTCTCTCTC	TCTCTCTCTC	TCTCTCTCTC	TCTCTCTCTC	TCTCTCTCTC	2400
CTCCCTCCCT	CCCTCTCTCT	CTCTTTGTGT	GCGTGTGTGG	TGGGGATGAG	GACACGTGTA	2460
GAACCTCGGG	GGTTGAGACT	TAGTGCATAT	GCATCCTCAC	CATTCCAGTT	AGTGAATGTT	2520
AACACTATTT	AAGGTCACAG	ACCTAACAGC	CTTCTGTGTC	CGGATTCCCTG	GATTCCCTAGG	2580
ACCTTTGTGG	ATGGGTTGCC	ACACCCTCTG	TGTTCATCCT	GACTGTGAGG	TCGATGGGAC	2640
ATAGTAGGGA	TAACTTTCAT	TTGGAATCTC	TAGAGATGGT	AGGTCACTCAT	GTCATAGAAT	2700
GTTATCACTA	ATGACCAAGA	TAGACACTCA	TGTTTAAGAG	ACATCACAAAG	GTGTATATTA	2760
AATATGACAT	GGCATATAAC	TTGTAATGAC	ACAAAAATAT	TCTGTTACCT	ACTTTCTCC	2820
AAAAAGCTTG	GGACTCTCCA	GAGTTCTAAA	TACATGCAA	CAGATTATTG	TGTTTACAG	2880
GAATCTTATA	TTGAACTTTC	TTTACCTGAC	TCAAATTATA	TTAAAATTAA	CTGGGAACAA	2940
ATAGTTGGTC	TCTAATCTCT	ACAAAAACCA	CCAAATGATT	ACACTGAGCA	TAATTATAAT	3000
CACCCCTGCTG	CTACGTCTAG	AAACCAAAC	GTGAAATATT	GGCTGACTGT	ATACCTTCCT	3060
AAATAATAAA	TTCAGGATAA	CATTGCCATA	TTATTGGAGA	ACCCCCCCC	CCCTTTTAAA	3120
ACTGGAATCA	TTTTATGTCA	ATCTCAGGTG	AAATACGAAT	GGGTTTCAGA	ACAGTGCTGT	3180
GCACTGAAGG	CTGACATTAA	GAACATATAT	AACGATTCT	GTAAAGTCTG	CTGTAACAAT	3240
TGCTGATTGT	ATCCTAGGAG	ACTTGGACTC	CTCTCAACGT	TAAGGCAGAG	GAATATAATG	3300
GTTATGAGAG	AAAAACTCTC	TGTCAGGTAC	ATCTGGCTTT	CTGTCCCAGC	TCTGTCACTT	3360
AAACACTTAGT	TGCGGTGGGA	AAACTCCCTG	ATCTTCCGGG	AGACTAAGTA	ACTGTATAAG	3420
CAAGCTGGCC	GTGATATCCA	CGTCGTAAGG	CTGCTGTGTG	GGTCAGTGA	AAACTGTTAC	3480
AGTGATTGGC	AGAGTTCTG	GAGGTCAATTG	ACCCCTCATTA	AACCTTGCAT	ACACTTATTG	3540
TTACTACTCT	TTGCTGTAG	TGTTGCCACC	AGGATTGCCA	TTCAAGGCAG	TCCTGTATAC	3600
TTGATAACAC	CAGTTGGTTC	TGAGGCCCTA	GTTAGCATCT	GTTAGCCTGG	TTCAGGAGAG	3660
TGTATCAGAG	CCAGGTTCCCT	CTATCACATA	AACTGTAACG	CAAGTGAATT	GTCCAATTGC	3720
TGTTGAGTCT	GAGAGTCCTT	GAGGTGCATA	GCTTTGACTA	ATAAAATCCCC	ATGCTTTTAT	3780
GCTTTCCCTT	CCTCCCTCTT	CCAGTTCAAC	ATCTAATATA	CAAAGATTGT	TCCGACCAC	3840
ACGTGCTAGG	AAGGAGAACG	AGTGGGGCCT	ACAGAGTTAC	CCCTGATCAC	AGAAACAGCA	3900
GCTTGAGGT	CTACTGTGAC	ATGGAGACCA	TGGGTGGAGG	CTGGACGGTG	CTGCAGGCTC	3960
GCCTTGATGG	CAGCACCAAC	TTCACCAGAG	AGTGGAAAGA	CTACAAAGCC	GGCTTTGGAA	4020
ACCTTGAACG	AGAATTTCGG	TTGGGCAACG	ATAAAATTCA	TCTCTGACC	AAGAGTAAGG	4080
AAATGATTTT	GAGAATAGAT	CTTGAAGACT	TTAATGGTCT	CACACTTTAT	GCCTTGTATG	4140
ATCAGTTTA	TGTGGCTAAT	GAATTCTCA	AAATACCGATT	ACACATCGGT	AACTACAATG	4200
GCACGGCAGG	GGATGCCTTG	CGTTTCAGTC	GACACTACAA	CCATGACCTG	AGGTTTTCA	4260
CAACCCCAGA	CAGAGACAAC	GATCGGTACC	CCTCTGGGAA	CTGTGGGCTC	TATTACAGCT	4320

- 70 -

CAGGCTGGTG	GTTTGATTCA	TGTCTCTCTG	CCAATTTAAA	TGGCAAATAT	TACCACCAGA	4380
AATACAAAGG	TGTCCGTAAT	GGGATTTCT	GGGGCACCTG	GCCTGGTATA	AACCAGGCAC	4440
AGCCAGGTGG	CTACAAGTCC	TCCTTCAAAC	AGGCCAAGAT	GATGATTAGG	CCCAAGAATT	4500
TCAAGCCATA	AATTGCTAGT	GTTCATCTCT	CTGGGCACTC	ACTATCTAAG	AGGACGATGA	4560
ATTCCCTTCAG	CCCTTTACCA	TATGTCTCAG	TTTATATTC	TTTCCTATGG	CTAAACATTT	4620
CCTTTAAAGC	TTTACAGCTT	TTAGAATAAA	GCTGAAAAGA	TCTAAAAGA	CTCCTATGTT	4680
GCTGTTATAT	GAGGAATGCT	TGAAAGCACT	GGAAATATTG	ACAATTATAC	ATTATAATTG	4740
CAAAACCTTT	CATTTTTATT	AGTGAAAAG	TTTCCTAATA	TTTTTATTAT	TTTTATAATA	4800
AAAACCTAAAT	TATTCAGCAA	GCTAGATTCT	ATATACGCAA	GTTCATTTT	CACTAGGGCT	4860
AAATATACAC	ATTTGAGAAT	ATACCAAGTCC	TTCCAGGTAC	AACTGAAAGC	CAAGAACTGT	4920
AGTATTATCT	TTCGTCTAAG	AAGAACCTAA	AGCATTCTAG	TTCTCAAGAA	GAAGGGCAGG	4980
GATGGGATTG	GGGGCCAGGG	ACAATATGTA	TAGCTAAATG	TATTCATCTA	ATGCAAATA	5040
TGGCATTAAA	ATACCTAAA	ATGTGGTAGC	ATAATATATG	TCTCTTCCCT	CTCCAATTGA	5100
AAAATAATGT	TACCCTGTAG	ACTTTGGTTT	AGTGGTAATT	CACTTACTGT	TTATAGCCTG	5160
TTAGACCGCG	ATACAAAAGC	TGCTTTATCC	TCTCCCTCTG	CTCTCTGTGC	ACAATGGTTT	5220
GTGATGTAAG	GTGCTAGACT	ACTGTAAGGT	TTCCCTGGGG	AAAGGCATGG	TAAGGGAAAA	5280
CACACTGGTT	TATATTTGA	AAGCCAATCC	TAATCCAAA	GCAATACTGT	TGTCGAGGAG	5340
TCAACGTTCT	AGGAAGCTGA	CTTTCTAGA	ACAAATGTAT	TTATTAGGAT	GAATTGGGA	5400
ATT						5403

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Arg	Leu	Pro	Gly	Trp	Leu	Trp	Leu	Ser	Ser	Ala	Val	Leu	Ala	Ala
1						5			10					15	

Cys	Arg	Ala	Val	Glu	Glu	His	Asn	Leu	Thr	Glu	Gly	Leu	Glu	Asp	Ala
								20	25				30		

Ser	Ala	Gln	Ala	Ala	Cys	Pro	Ala	Arg	Leu	Glu	Gly	Ser	Gly	Arg	Cys
					35			40				45			

Glu	Gly	Ser	Gln	Cys	Pro	Phe	Gln	Leu	Thr	Leu	Pro	Thr	Leu	Thr	Ile
					50			55			60				

Gln	Leu	Pro	Arg	Gln	Leu	Gly	Ser	Met	Glu	Glu	Val	Leu	Lys	Glu	Val
				65			70			75			80		

- 71 -

Arg Thr Leu Lys Glu Ala Val Asp Ser Leu Lys Lys Ser Cys Gln Asp
85 90 95

Cys Lys Leu Gln Ala Asp Asp His Arg Asp Pro Gly Gly Asn Gly Gly
100 105 110

Asn Gly Ala Glu Thr Ala Glu Asp Ser Arg Val Gln Glu Leu Glu Ser
115 120 125

Gln Val Asn Lys Leu Ser Ser Glu Leu Lys Asn Ala Lys Asp Gln Ile
130 135 140

Gln Gly Leu Gln Gly Arg Leu Glu Thr Leu His Leu Val Asn Met Asn
145 150 155 160

Asn Ile Glu Asn Tyr Val Asp Asn Lys Val Ala Asn Leu Thr Val Val
165 170 175

Val Asn Ser Leu Asp Gly Lys Cys Ser Lys Cys Pro Ser Gln Glu His
180 185 190

Met Gln Ser Gln Pro Val Gln His Leu Ile Tyr Lys Asp Cys Ser Asp
195 200 205

His Tyr Val Leu Gly Arg Arg Ser Ser Gly Ala Tyr Arg Val Thr Pro
210 215 220

Asp His Arg Asn Ser Ser Phe Glu Val Tyr Cys Asp Met Glu Thr Met
225 230 235 240

Gly Gly Gly Trp Thr Val Leu Gln Ala Arg Leu Asp Gly Ser Thr Asn
245 250 255

Phe Thr Arg Glu Trp Lys Asp Tyr Lys Ala Gly Phe Gly Asn Leu Glu
260 265 270

Arg Glu Phe Trp Leu Gly Asn Asp Lys Ile His Leu Leu Thr Lys Ser
275 280 285

Lys Glu Met Ile Leu Arg Ile Asp Leu Glu Asp Phe Asn Gly Leu Thr
290 295 300

Leu Tyr Ala Leu Tyr Asp Gln Phe Tyr Val Ala Asn Glu Phe Leu Lys
305 310 315 320

Tyr Arg Leu His Ile Gly Asn Tyr Asn Gly Thr Ala Gly Asp Ala Leu
325 330 335

Arg Phe Ser Arg His Tyr Asn His Asp Leu Arg Phe Phe Thr Thr Pro
340 345 350

Asp Arg Asp Asn Asp Arg Tyr Pro Ser Gly Asn Cys Gly Leu Tyr Tyr
355 360 365

Ser Ser Gly Trp Trp Phe Asp Ser Cys Leu Ser Ala Asn Leu Asn Gly
370 375 380

Lys Tyr Tyr His Gln Lys Tyr Lys Gly Val Arg Asn Gly Ile Phe Trp
385 390 395 400

Gly Thr Trp Pro Gly Ile Asn Gln Ala Gln Pro Gly Gly Tyr Lys Ser
405 410 415

Ser Phe Lys Gln Ala Lys Met Met Ile Arg Pro Lys Asn Phe Lys Pro
420 425 430